

Tutorial 6: GeneList – An important concept in ArrayTrack



Introduction

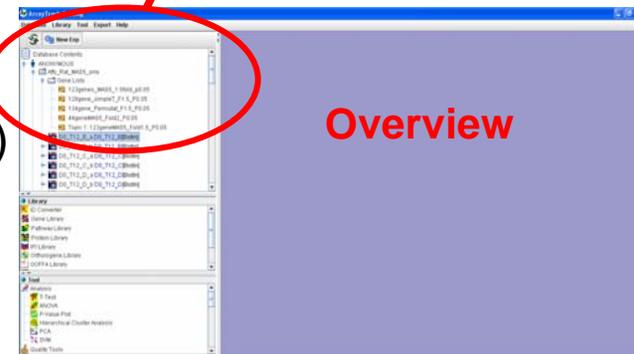
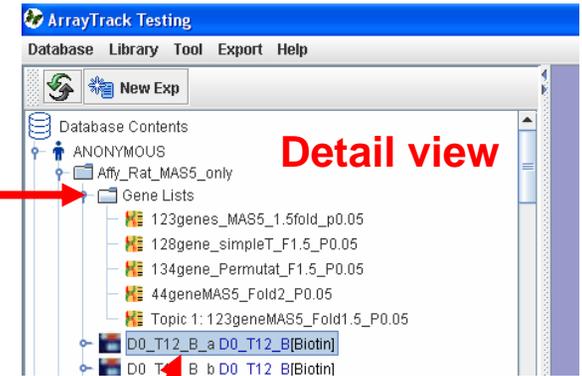
The Gene List folder contains gene lists that are usually derived from applying certain filtering criteria (e.g. P-value, fold change, etc) on the microarray data. As a common practice, a list of gene is identified by researchers and then carried forward for biological interpretation and/or further analysis.

There are several ways to create a gene list in ArrayTrack:

- Create a gene list through statistical analysis (page 3)
- Create a gene list through data filtering (page 5)
- Create a gene through manual selection (page 6)
- Alternatively, the user can import a list of genes that is created outside of ArrayTrack. (page 7)

ArrayTrack allows the following operations solely based on gene lists:

- Normalization based on a gene list (page 14)
- Statistical analysis (t-test, PCA, HCA) applied on a gene list (page 15)
- Venn diagram drawn on two or three gene lists (page 12)
- Functional analysis on a gene list (page 19)
- Export a set of microarray with genes that are specified by a gene list (page 21)
- Miscellaneous: delete a gene list (page 9); create a Gene List subfolder (page 22)



Create a gene list through statistical analysis

1. From data analysis results (e.g. T-test result. See Tutorial 1 for doing T-test).

The screenshot displays the 'T-Test Results' window. The main table lists 19 genes with columns for Genbank Acc, Gene Mfr ID, LOCUSID, GENENAME, REFSEQ, SPOTID, P, Abs Fold C..., Fold Chang..., Total Bad Fl..., Grp 1 Size, Grp 2 Size, and Bad F. The P-values are highlighted in blue. A red box labeled 'T-test result' encloses the table. Below the table, the 'Significance Filtering' panel is visible, showing options for P Values (set to 0.05), Target False Discovery Rate (FDR), Select # genes, Mean Channel Intensities, and Abs Fold Change (set to 1.5). A red box labeled 'Set P value and fold change criteria' points to the P value and Abs Fold Change fields. Another red box labeled 'Click "Create Sig. Gene List" button' points to the 'Create Sig. Gene List' button at the bottom. The bottom of the window shows buttons for 'P-Value Plot', 'Create Sig. Gene List', 'HCA', 'PCA', and 'Volcano Plot'.

	Genbank Acc	Gene Mfr ID	LOCUSID	GENENAME	REFSEQ	SPOTID	P	Abs Fold C...	Fold Chang...	Total Bad Fl...	Grp 1 Size	Grp 2 Size	Bad F
1	AA108277	AA108277_...	288444	Hsp105_pr...		516484	0.6801	1.1422	1.1422	0	2	2	0
2	AA108308	AA108308_...	314856			516485	0.9155	1.036	1.036	4	2	2	2
3	AA108308	AA108308_...				516486	0.2315	1.4239	0.7023	0	2	2	0
4	AA684537	AA684537_...	294964	Ndufb5_pr...		516487	0.6331	1.1285	0.8861	4	2	2	2
5	AA684929	AA684929_...				516488	0.0892	1.4882	0.672	4	2	2	2
6	AA684960	AA684960_...				516489	0.3848	1.7996	0.5557	4	2	2	2
7	AA684963	AA684963_...	293702	LOC293702		516490	0.5062	1.1965	1.1965	0	2	2	0
8	AA685112	AA685112_...	293652	Ndufs8_pr...		516491	0.2692	1.2343	1.2343	0	2	2	0
9	AA685152	AA685152_...	25490	Nedd8		516492	0.1367	1.9005	1.9005	0	2	2	0
10	AA685376	AA685376_...				516493	0.069	2.3412	0.4271	4	2	2	2
11	AA685876	AA685876_...	304805	Nqo3a2_pr...		516494	0.2984	1.2289	0.8137	4	2	2	2
12	AA685903	AA685903_...	362862	Tra1_predi...		516495	0.9871	1.0047	1.0047	0	2	2	0
13	AA686031	AA686031_...	301458	Ndufs1		516496	0.956	1.007	0.993	0	2	2	0
14	AA686579	AA686579_...	301442	Sumo1_pr...		516497	0.6683	1.123	1.123	0	2	2	0
15	AA686870	AA686870_...				516498	0.8915	1.1977	0.8349	4	2	2	2
16	AA686870	AA686870_...				516499	0.4097	8.8764	0.1127	4	2	2	2
17	AA799336	AA799336_...	293453	Ndufab1_p...		516500	0.8428	1.0395	1.0395	0	2	2	0
18	AA819943	AA819943_...				516501	0.2473	2.3581	0.4241	4	2	2	2
19	AA848218	AA848218_...	64550	Top1		516502	0.3299	1.5149	1.5149	0	2	2	0

1031 genes

Significance Filtering

P Values without adjustment

Target False Discovery Rate (FDR):

Select # genes by lowest p-values

Mean Channel Intensities > Bad Flags <=

Abs Fold Change > Advanced>>

Apply Filters Clear Filters

P-Value Plot Create Sig. Gene List HCA PCA Volcano Plot

Create a gene list through statistical analysis - continued

Create Gene List

Create gene list named: Type Gene List Name Here

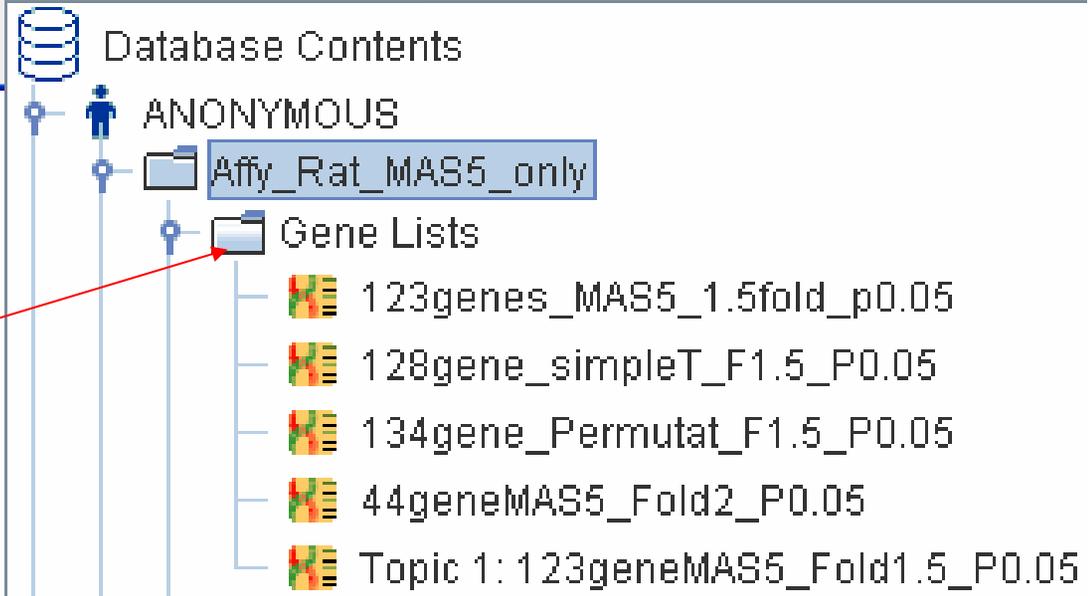
Save into experiment: Affy_Rat_MAS5_only

Under gene list group (optional):

Description
describe the gene list

OK Cancel

Can be saved into different experiment



The saved gene list will be displayed under the experiment

Create a gene list through data filtering

User can set the criteria (like flag, intensity value) to create a gene list, e.g find out all the genes which intensity is greater than 3.0 in at least 6 out of 12 hybridizations.

The total number of selected hybridizations

Database Contents
ANONYMOUS
Affy_Rat_MAS5_only
Gene Lists
D0_T12_B_a D0_T12_B[Biotin]
MAS5 {D0_T12_B_a} [file: ...]
Mean/Median Scaling,
D0_T12_B_b D0_T12_B[Biotin]
MAS5 {D0_T12_B_b} [file: ...]
Mean/Median Scaling,
D0_T12_C_a D0_T12_C[Biotin]
MAS5 {D0_T12_C_a} [file: ...]
Mean/Median Scaling,
D0_T12_C_b D0_T12_C[Biotin]
MAS5 {D0_T12_C_b} [file: ...]
Mean/Median Scaling,
D0_T12_D_a D0_T12_D[Biotin]
MAS5 {D0_T12_D_a} [file: ...]

Right-click the selected data, choose "Create gene list by data filtering"

Create Gene List

Intensities: Require at least of the

Flags: Require at least of the in list

Resulting Gene List Name:

Auto-append filters summary to name

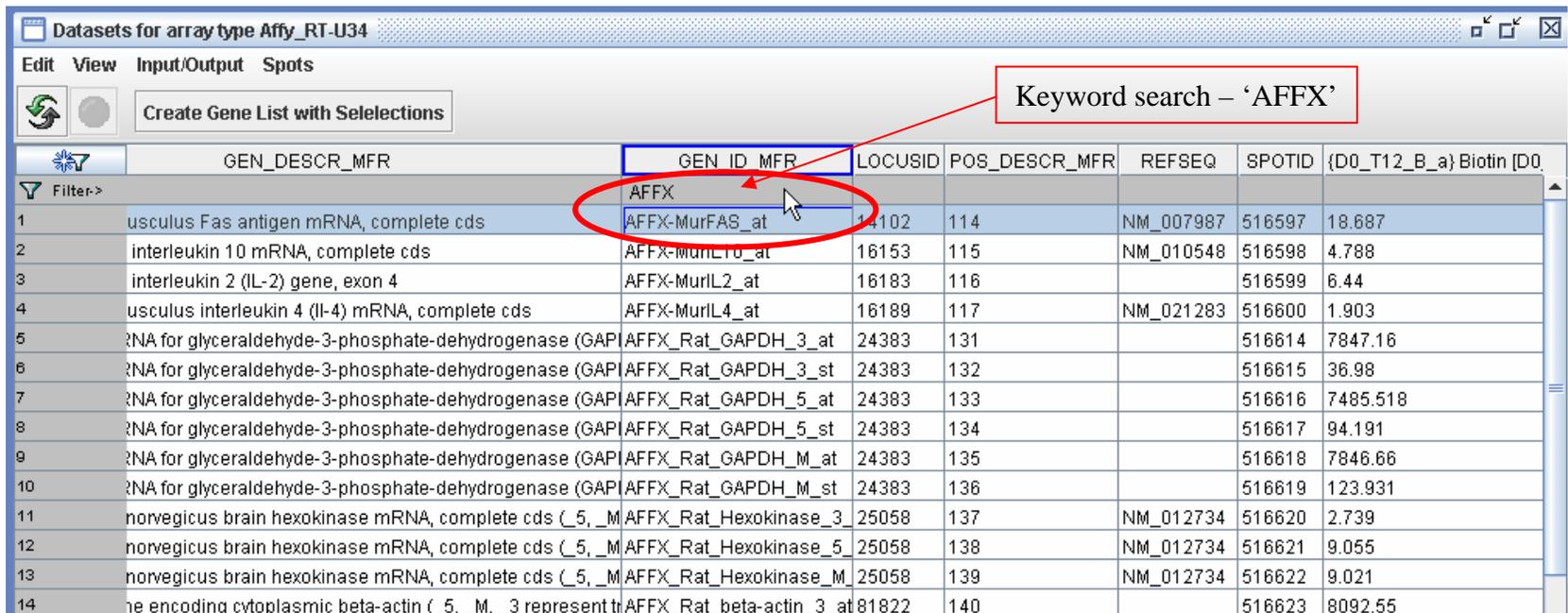
Place in Gene List Group (optional):

OK Cancel

- View data set(s) as wide spreadsheet - datasets side by side
- Export
- Convert affy cel files to probe sets
- Mixed scatterplot
- Virtual array images for data
- Actual array images for data <<Dev. Only>>
- Rank intensity plots for data
- BarChart
- Create gene list by data filtering...**
- Analysis

Create a gene list through manually selection

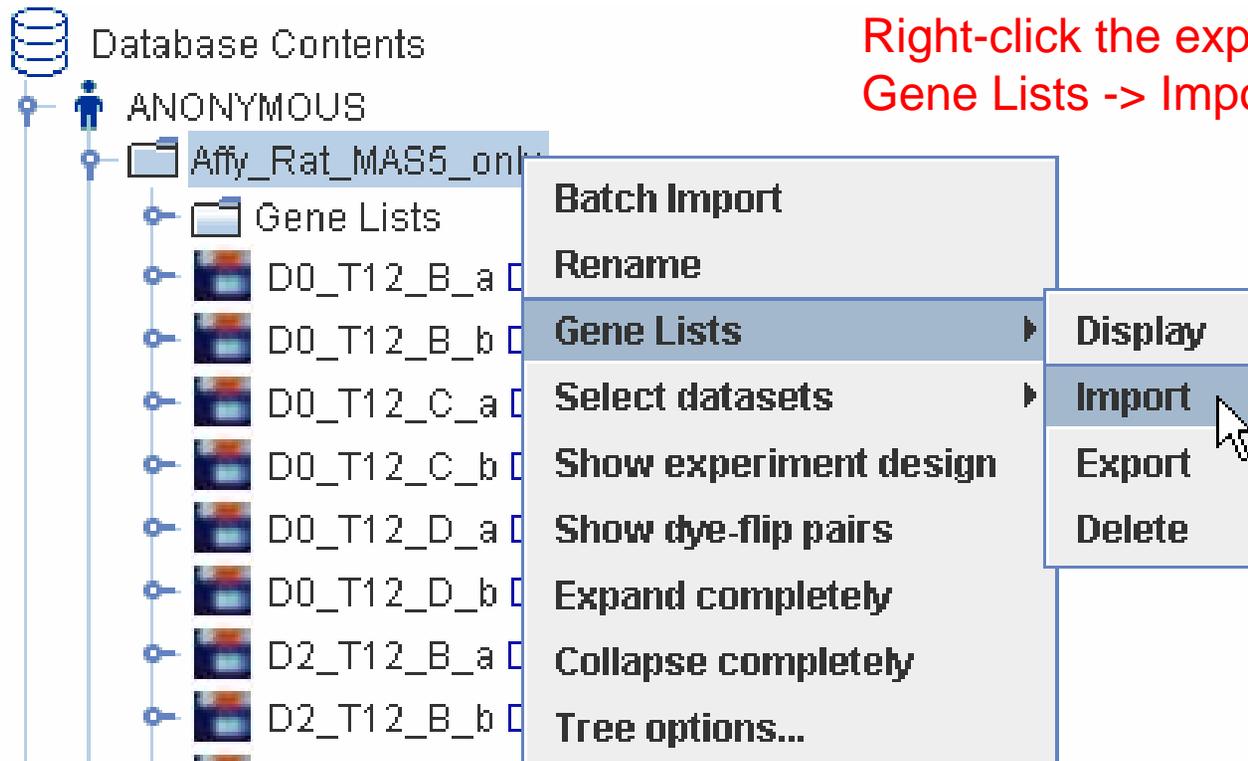
2. The user can filter out some genes (e.g. spike-in genes) to get a gene list for further normalization.



Keyword search – ‘AFFX’

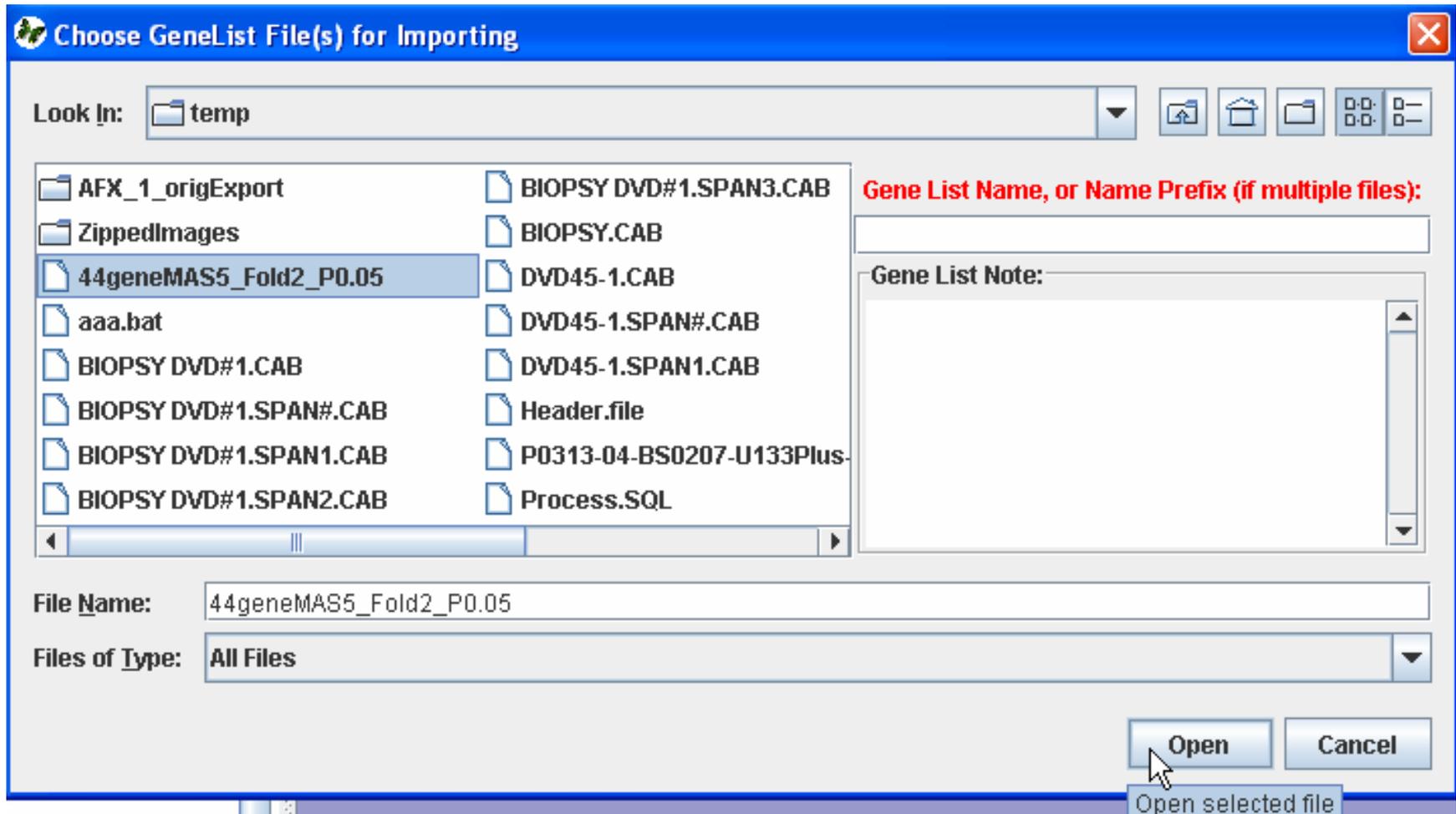
	GEN_DESCR_MFR	GEN_ID_MFR	LOCUSID	POS_DESCR_MFR	REFSEQ	SPOTID	{D0_T12_B_a} Biotin [D0
Filter->		AFFX					
1	usculus Fas antigen mRNA, complete cds	AFFX-MurFAS_at	14102	114	NM_007987	516597	18.687
2	interleukin 10 mRNA, complete cds	AFFX-MurIL10_at	16153	115	NM_010548	516598	4.788
3	interleukin 2 (IL-2) gene, exon 4	AFFX-MurIL2_at	16183	116		516599	6.44
4	usculus interleukin 4 (IL-4) mRNA, complete cds	AFFX-MurIL4_at	16189	117	NM_021283	516600	1.903
5	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_3_at	24383	131		516614	7847.16
6	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_3_st	24383	132		516615	36.98
7	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_5_at	24383	133		516616	7485.518
8	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_5_st	24383	134		516617	94.191
9	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_M_at	24383	135		516618	7846.66
10	?NA for glyceraldehyde-3-phosphate-dehydrogenase (GAPD	AFFX_Rat_GAPDH_M_st	24383	136		516619	123.931
11	norvegicus brain hexokinase mRNA, complete cds (_5, _M	AFFX_Rat_Hexokinase_3	25058	137	NM_012734	516620	2.739
12	norvegicus brain hexokinase mRNA, complete cds (_5, _M	AFFX_Rat_Hexokinase_5	25058	138	NM_012734	516621	9.055
13	norvegicus brain hexokinase mRNA, complete cds (_5, _M	AFFX_Rat_Hexokinase_M	25058	139	NM_012734	516622	9.021
14	he encoding cytoplasmic beta-actin (_5, _M, _3 represent	AFFX_Rat_beta-actin_3_at	81822	140		516623	8092.55

Import/Export a gene list



Right-click the experiment, then choose
Gene Lists -> Import

Import/Export a gene list – cont.



Import/Export a gene list – cont.

Choose Columns

Field Separator:

genebankacc	genename	locusid	unigeneid	swissprot_acc_number	description	expression_level1	expression_level2
AI011376	Mapkapk3_...	315994		Q66H84			
X57523	Tap1	24811		P36370 /// P97559 /// P97...			
X94185	Dusp6	116663		Q64346			
AA999168	Ndufb8_pre...	293991					
U03491	Tgfb3	25717		Q07258 /// Q56A31			
M22899	Ii2	116562		P17108			
AJ223083	Rxrg	83574		O70464 /// Q9Z2U7 /// Q5...			
D84667	Pik4cb	81747		O08561			
X56420	Mpg	24561		P23571			
L25925	Ptgs2	29527		P35355 /// Q63124 /// Q8...			
J05181	Gclc	25283		P19468			
AI169708	Ugt2b	24862		P08541 /// Q5EBC8			
AFO31657	Zfp94	199095					

For each column description below, select a table column above and click the description button to make the assignment.

<input checked="" type="checkbox"/>	ArrayTrack SPOT ID	<input checked="" type="checkbox"/>	Assigned to spotid (19)
<input checked="" type="checkbox"/>	Manufacture ID	<input checked="" type="checkbox"/>	Assigned to gen_id_mfr (17)
<input checked="" type="checkbox"/>	GeneBankAcc	<input checked="" type="checkbox"/>	Assigned to genebankacc (3)
<input checked="" type="checkbox"/>	Ref Seq	<input checked="" type="checkbox"/>	Assigned to refseq (20)
<input checked="" type="checkbox"/>	GeneName	<input checked="" type="checkbox"/>	Assigned to genename (4)
<input checked="" type="checkbox"/>	LocusID	<input checked="" type="checkbox"/>	Assigned to locusid (5)
<input checked="" type="checkbox"/>	UnigeneID	<input checked="" type="checkbox"/>	Assigned to unigeneid (6)
<input checked="" type="checkbox"/>	SwissProtAcc	<input checked="" type="checkbox"/>	Assigned to swissprot_acc_number (7)

OK Cancel

Assign table columns to the corresponding fields

Import/Export a gene list - continued

The screenshot displays a database interface with a tree view on the left and a context menu on the right. The tree view shows the following structure:

- Database Contents
 - ANONYMOUS
 - Affy_Rat_MAS5_only
 - Gene Lists
 - 128gene_simpleT_F1.5_P0.05 (highlighted)
 - 134gene_Permutat_F1.5_P0.0
 - 44geneMAS5_Fold2_P0.05
 - Topic 1: 123geneMAS5_Fold1.5
 - D0_T12_B_a D0_T12_B[Biotin]
 - D0_T12_B_b D0_T12_B[Biotin]
 - D0_T12_C_a D0_T12_C[Biotin]
 - D0_T12_C_b D0_T12_C[Biotin]

The context menu is open over the highlighted gene list, showing the following options:

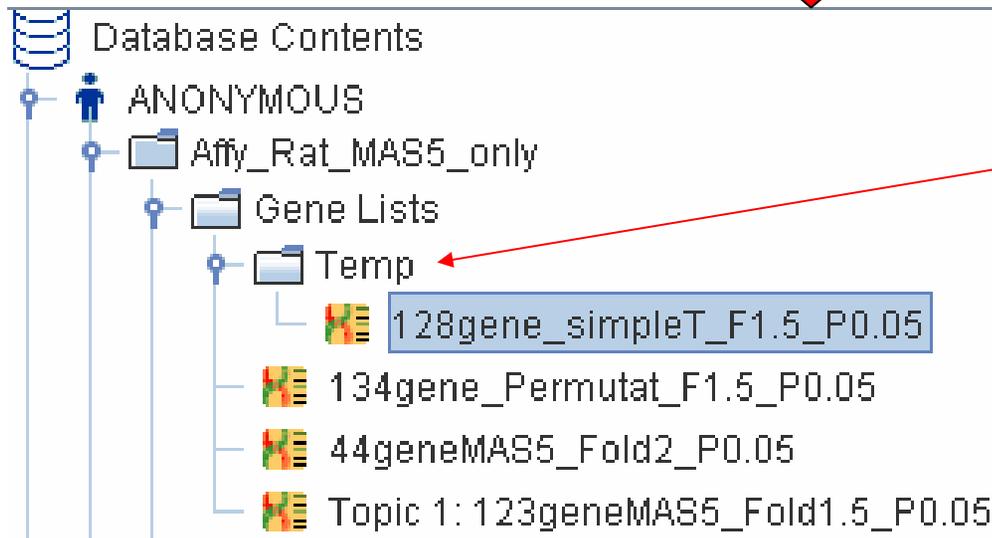
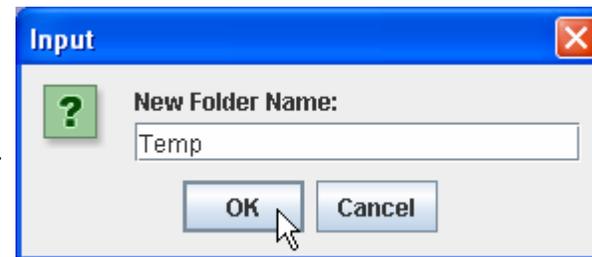
- Open
- Export** (circled in red)
- Rename
- Delete
- Move To (New) Folder** (circled in red)
- Move Out Folder
- Copy Genelist For Pasting Elsewhere

Annotations with red arrows point to specific menu items:

- An arrow points from the **Export** item to a text box containing "Export the gene list".
- An arrow points from the **Move To (New) Folder** item to a text box containing "Move the gene list To a new folder See next slide".

Import/Export a gene list - continued

Move gene list to a new folder



The gene is moved to new Folder - Temp

Import/Export a gene list - continued

The screenshot displays a database interface with a tree view of 'Database Contents'. Under 'ANONYMOUS', there is a folder 'Affy_Rat_MAS5_only' containing a sub-folder 'Gene Lists'. A context menu is open over a selected gene list file. The menu items are: Open, Export, Rename, Delete, Move To (New) Folder, Move Out Folder, and Copy Genelist For Pasting Elsewhere. Red boxes and arrows highlight the 'Rename' and 'Delete' options, with text labels 'Rename the gene list' and 'Delete the gene list' pointing to them.

Database Contents

- ANONYMOUS
 - Affy_Rat_MAS5_only
 - Gene Lists
 - 123genes_MAS5_1.5fold_p0.05
 - 128gene_simpleT_F1.5_P
 - 134gene_Permutat_F1.5_F
 - 44geneMAS5_Fold2_P0.05
 - Topic 1: 123geneMAS5_Fol

Context Menu:

- Open
- Export
- Rename
- Delete
- Move To (New) Folder
- Move Out Folder
- Copy Genelist For Pasting Elsewhere

Annotations:

- Rename the gene list
- Delete the gene list

Draw Venn Diagram from gene lists

The image shows a screenshot of a database management system interface. On the left, a tree view displays the following structure:

- Database Contents
 - ANONYMOUS
 - Affy_Rat_MAS5_only
 - Gene Lists
 - 123genes_MAS5_1.5fold_p0.05
 - 128gene_simpleT_F1.5_P0.05
 - 134gene_Permutat_F1.5_P0.05
 - 44geneMAS5_Fold2_P0.05
 - Topic 1: 123geneMAS5_Fold1.5
 - D0_T12_B_a D0_T12_B[Biotin]
 - D0_T12_B_b D0_T12_B[Biotin]
 - D0_T12_C_a D0_T12_C[Biotin]
 - D0_T12_C_b D0_T12_C[Biotin]
 - D0_T12_D_a D0_T12_D[Biotin]
 - D0_T12_D_b D0_T12_D[Biotin]
 - D2_T12_B_a D2_T12_B[Biotin]
 - D2_T12_B_b D2_T12_B[Biotin]
 - D2_T12_C_a D2_T12_C[Biotin]

A context menu is open over the 'Gene Lists' folder, with the following options:

- Open
- Export
- Rename
- Delete
- Move To (New) Folder
- Move Out Folder
- Copy Genelist For Pasting Elsewhere
- VennDiagram
 - By CommonID
 - By Pathway
 - By GeneOntology

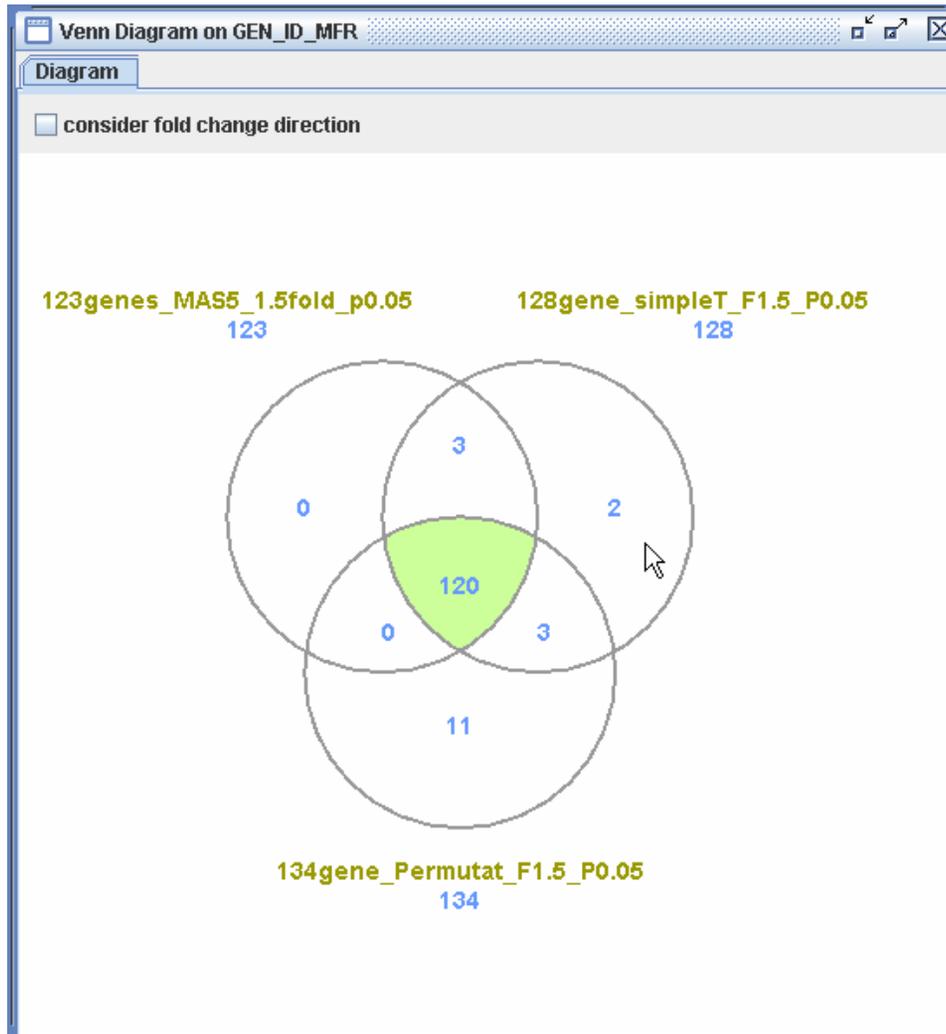
The 'VennDiagram' sub-menu is further expanded, showing the following options:

- Manufacture ID
- Locus ID
- GeneName
- GeneBankAcc
- REFSEQ
- Spot ID

Three red boxes with arrows point to specific elements in the interface:

- The first box, labeled "Select gene lists", points to the 'Gene Lists' folder in the tree view.
- The second box, labeled "Draw Venn Diagram By different approach", points to the 'VennDiagram' option in the context menu.
- The third box, labeled "Draw Venn Diagram By various ID", points to the 'Manufacture ID' option in the sub-menu.

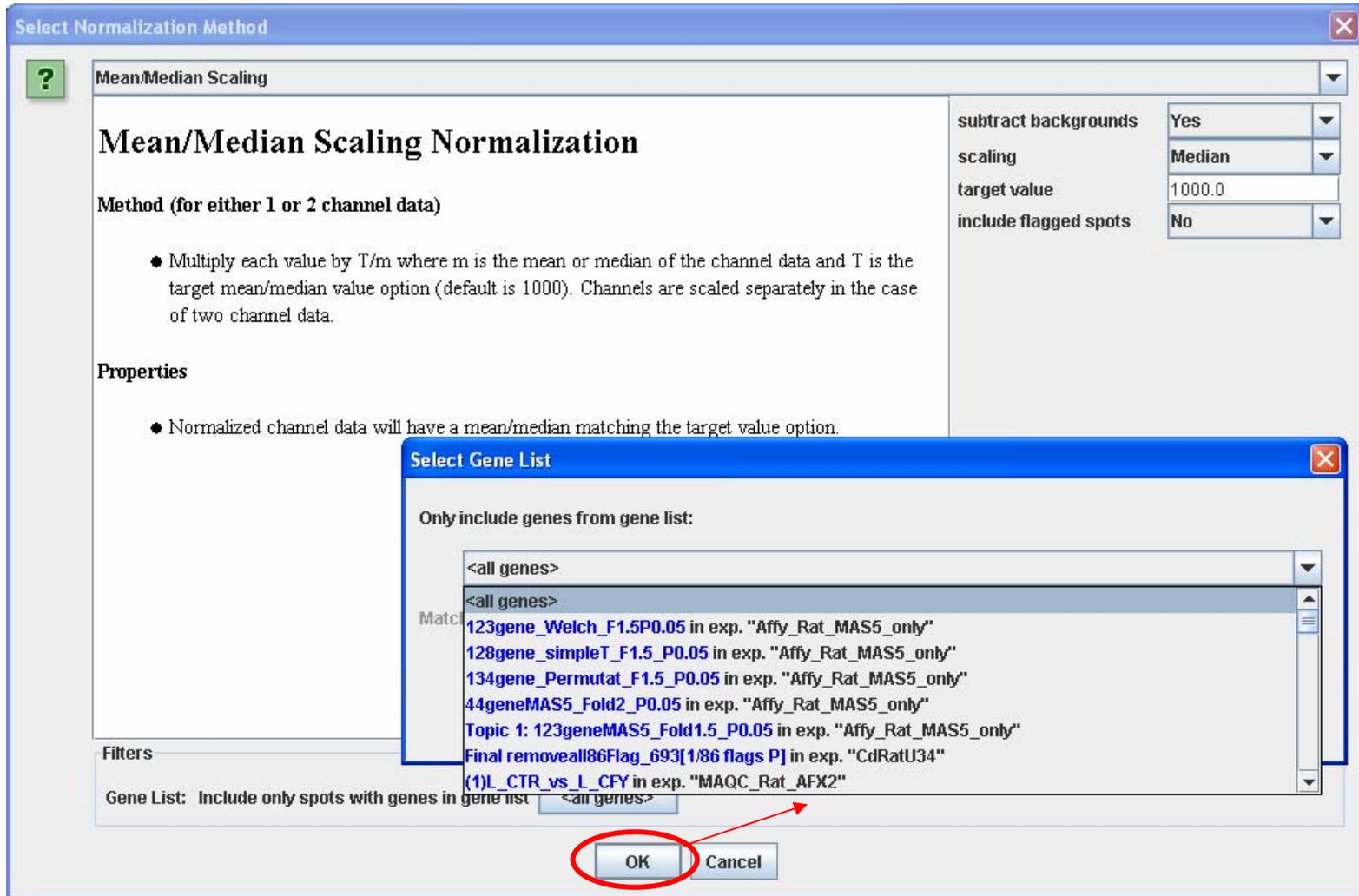
Draw Venn Diagram from gene lists -continued



More detail about Venn Diagram
Is explained in Tutorial 3.

Conduct normalization filtered by a gene list

User can do data normalization based on a filtered gene list. Refer tutorial 7 for Normalization methods.



Conduct statistical analysis based on a gene list

Select Dataset Group Assignments for T-Test / ANOVA / Pairwise Tests

Test Type (Consistent with group selections)

T-Test

T-Test Options

P values from dist.: Welch t-test Simple t-test One class vs. mean:

P values from permutations: All Limit to:

Filtering with a gene list

Only include genes from gene list: **<all genes>**

Gene identifiers to include

Genbank Acc Gene Mfr ID LOCUSID UNIGENEID GENENAME

CLONEID GEN_DESCR_MFR REFSEQ SPOTID

Dataset Naming

Hybridization names are always included.

add sample name(s) to hybridization names

add dye name(s) to hybridization names

Data options

Subtract backgrounds when present (raw datasets only)

Apply log (base 2) to expression values

Exclude spots flagged as bad

< Back Do Tests

Doing T-test based on a filtered gene lists
Refer tutorial 1 for T-test

Select Gene List

Only include genes from gene list:

<all genes>

Match

123gene_Welch_F1.5P0.05 in exp. "Affy_Rat_MAS5_only"

128gene_simpleT_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

134gene_Permutat_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

44geneMAS5_Fold2_P0.05 in exp. "Affy_Rat_MAS5_only"

Topic 1: 123geneMAS5_Fold1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

Final removeall86Flag_693[1/86 flags PJ] in exp. "CdRatU34"

(1)L_CTR_vs_L_CFY in exp. "MAQC_Rat_AFX2"

Conduct statistical analysis based on a gene list - continued

Doing PCA based on a filtered gene lists. Refer Tutorial 4 for PCA

PCA Options

Centered Auto scaled

Gene List Filtering

Only include genes from gene list:

Match: <all genes>

Data: <all genes>

Hybridization: add dye name(s) to hybridization names

123gene_Welch_F1.5P0.05 in exp. "Affy_Rat_MAS5_only"

128gene_simpleT_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

134gene_Permutat_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

44geneMAS5_Fold2_P0.05 in exp. "Affy_Rat_MAS5_only"

Topic 1: 123geneMAS5_Fold1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

Final removeall86Flag_693[1/86 flags P] in exp. "CdRatU34"

(1)L_CTR_vs_L_CFY in exp. "MAQC_Rat_AFX2"

Ok Cancel

Conduct statistical analysis based on a gene list - continued

Create Correlation Matrix

Edit Datasets Groups Gene Id's Data-Options

Groups: Assign to New Group Unassign Assign to... Clear All Groups

	Hybridization	SAMPLE 1	LABEL 1	SAMPLE 2	LABEL 2	ARRAYTYPENAME	LA
1	①	Strain A Q380	Strain A - mice 1	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh
2	①	Strain A Q381	Strain A - mice 2	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh
3	①	Strain A Q382	Strain A - mice 3	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh
4	②	Strain B Q385	Strain B - mice 1	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh
5	②	Strain B Q386	Strain B - mice 2	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh
6	②	Strain B Q387	Strain B - mice 3	Cy5	Reference	Cy3	NCTR_MWG_MouseJoh

2 groups, sizes = [3, 3]

Above you may *optionally* assign datasets into groups here, w separated visually in the output matrix.
Note: If any group assignments are made, then any datasets r a group will ignored.

Only include genes from gene list:

Doing Correlation Matrix based on a filtered gene list Refer Tutorial 10 for Correlation Matrix

Select Gene List

Only include genes from gene list:

- <all genes>
- <all genes>
- Match 174Welch_t_2fold_p0.05 in exp. "Strain_mice_two_Channel"
- 187Welch_t_1.5fold_p0.01 in exp. "Strain_mice_two_Channel"
- 187gene_P0.01_F1.5 in exp. "Strain_mice_two_Channel"
- 198protein_P0.01 in exp. "Strain_mice_two_Channel"
- 202Welch_t_test_P0.005 in exp. "Strain_mice_two_Channel"
- 206simple_t-tset_2fold_p0.05 in exp. "Strain_mice_two_Channel"
- 25chemicals_Lino_Terp.xls in exp. "Strain_mice_two_Channel"

Conduct statistical analysis based on a gene list - continued

Doing HCA based on a filtered gene list
Refer Tutorial 4 for HCA

HCA Options

Auto scale data Cluster sorted by value

Method Selection

Dual cluster Heat map (no clustering)

Distance

Manhattan Euclidean 1- τ

LinkageType

Single Complete Average Centroid Median Ward's

Gene List Filtering

Only include genes from gene list:

Match

Data

Hybridization

add dye name(s) to hybridization names

25chemicals_Lino_Terp.xls in exp. "Strain_mice_two_Channel"

174Welch_t_2fold_p0.05 in exp. "Strain_mice_two_Channel"

187Welch_t_1.5fold_p0.01 in exp. "Strain_mice_two_Channel"

187gene_P0.01_F1.5 in exp. "Strain_mice_two_Channel"

198protein_P0.01 in exp. "Strain_mice_two_Channel"

202Welch_t_test_P0.005 in exp. "Strain_mice_two_Channel"

206simple_t-tset_2fold_p0.05 in exp. "Strain_mice_two_Channel"

<all genes>

<all genes>

Ok Cancel

Biological interpretation using ArrayTrack Pathway, GO and other tools

Individual gene
annotation and analysis

Pathway analysis

GO-based
functional analysis

The screenshot displays the ArrayTrack Testing interface. On the left, the 'Database Contents' pane shows a tree structure under 'Afry_Rat_MAS5_only' with 'Gene Lists' containing 'Topic 1: 123geneMAS5_Fold1.5_P0.05'. A red circle highlights this entry with the text 'Double click'. The main window shows a table titled 'SIGNIFICANT_GENELIST' with columns: GENELIST_NAME *, EXPID *, KEGG, NAME, LOCUSID, FOLD, and PVALUE. A dropdown menu is open over the 'Pathways' button, listing options: PathArt, Ingenuity, and GeneGo MetaCore. Red arrows point from the text labels above to the 'Genes', 'Pathways', and 'GOFA' buttons.

GENELIST_NAME *	EXPID *	KEGG	NAME	LOCUSID	FOLD	PVALUE
1	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	predicted	288444	4.1286	0.0006
2	Topic 1: 123geneMAS5_Fold1.5_P0.0	650		300721	5.3215	0.0038
3	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Hspat17/Hspa1b		14.9075	0.0003
4	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Dao1	114027	0.6656	0.0107
5	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Cdc42bpa	114116	0.4238	0.0184
6	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Casp6	83584	0.2951	0.0161
7	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Casp6	83584	0.4238	0.0149
8	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Zfp94	499095	0.4941	0.0203
9	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Nme6	58964	0.5452	0.0282
10	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Nme6	58964	0.2628	0.0145
11	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Taok1	286993	0.5826	0.0092
12	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Mapk7	114509	0.5151	0.0082
13	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Mer2d	81518	0.5585	0.0121
14	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Rxrg	83574	2.5979	0.0285
15	Topic 1: 123geneMAS5_Fold1.5_P0.0	650	Ccnd1	58919	0.6225	0.0065

Individual gene annotation and analysis using GeneLib

Summary info for the highlighted gene

Link to other pub databases for the highlighted gene

The screenshot displays the GeneLib software interface. On the left, there is a search panel with options for 'Specify ID Type' (GenBankAcc, UnigenID, LocusID, SwissProtAcc, IMAGEID, GEN_ID_MFR, GeneName) and 'Enter Searching Data' with a search button. The main window shows a table of search results. The table has columns for 'Filter->', 'geneid as INPUT LOCUSID', 'GENENAME', 'DESCRIPTION', and 'Link To'. Row 7 is highlighted, showing the gene 'Mpg' (N-methylpurine-DNA glycosylase). Two dropdown menus are open over the 'Link To' column for the highlighted row, showing options like 'Gene Synonyms', 'Gene Summary', 'Gene Ontology', 'NCBI RefSeq', 'GenBank Access', 'Pathway', 'Protein Synonym', 'EntrezGene', 'Unigene', 'OMIM', 'GeneCard', 'Chromosomal Map', 'SwissProt', and 'GDB'. A message box at the bottom left shows a unique search ID number of 91.

Filter->	geneid as INPUT LOCUSID	GENENAME	DESCRIPTION	Link To
1	24296	Cyp1a1	cytochrome P450, family 1, subfamily A, member 1	R:
2	24404	Gpx1	glutathione peroxidase 1	R:
3	24451	Hmox1	heme oxygenase (decipherase)	R:
4	24471	Hspb1	heat shock protein 70 kDa class B member 1	R:
5	24472	Hspa1a	heat shock protein 70 kDa class A member 1	R:
6	24553	Met	methionine synthase	R:
7	24561	Mpg	N-methylpurine-DNA glycosylase	R:
8	24565	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	R:
9	24567	Mt1a	Metallothionein	R:
10	24605	Nras	neuroblastoma RAS viral (v-ras) oncogene homolog	R:
11	24646	Abcb1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	R:
12	24811	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	R:
13	24842	Tp53	tumor protein p53	R:
14	24862	Ugt2b	UDP glycosyltransferase 2 family, polypeptide B	R:
15	24891	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	R:
16	25035	Dia1	diaphorase 1	R:
17	25283	Gclc	glutamate-cysteine ligase, catalytic subunit	R:
18	25315	Ephx1	epoxide hydrolase 1	R:
19	25355	Ste	sulfotransferase, estrogen preferring	R:
20	25406	Cd44	CD44 antigen	R:
21	25420	Cryab	crystallin, alpha B	R:
22	25493	Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha 1	R:
23	25591	Adprt	ADP-ribosyltransferase 1	R:
24	25625	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	R:
25	25675	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	R:
26	25717	Tgfb3	transforming growth factor, beta 3	R:
27	26759	Bach	brain acyl-CoA hydrolase	R:
28	26844	Tfcp2l1	tear factor protein 26, C2H-type like 1	R:

Export a dataset by specifying the gene list

The user can export data with only selected genes. Refer Tutorial 9 for data export.

The screenshot displays a software interface with a tree view on the left and a menu on the right. The tree view shows a project named 'Affy_Rat_MAS5_only' with several sub-items, including 'Gene Lists' and multiple 'MAS5' datasets. The 'Export' menu is open, showing options like 'Export single-platform data as spreadsheet' (highlighted with a red box) and 'Export gene-matched data as spreadsheet (multi-platform OK)'. An 'Export Options' dialog box is overlaid on the right, with the 'Gene Filtering' tab selected (circled in red). The dialog box contains a list of gene filters, with '123genes_MAS5_1.5fold_p0.05 in exp. "Affy_Rat_MAS5_only"' selected. The dialog also has 'OK' and 'Cancel' buttons at the bottom.

Export Options

Output Options

Intensity Data Fields Dataset Filtering **Gene Filtering** Spot Fields Dataset Naming

Only include genes from gene list:

<all genes>

<all genes>

123genes_MAS5_1.5fold_p0.05 in exp. "Affy_Rat_MAS5_only"

128gene_simpleT_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

134gene_Permutat_F1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

44geneMAS5_Fold2_P0.05 in exp. "Affy_Rat_MAS5_only"

Topic 1: 123geneMAS5_Fold1.5_P0.05 in exp. "Affy_Rat_MAS5_only"

Match Final removeall86Flag_693[1.86 flags P] in exp. "CdRatU34"

[4/6 ints >= 10] in exp. "Strain_mice_two_Channel"

SPOTID

OK Cancel